
Sequence Listing was accepted.

If you need help call the Patent Electronic Business Center at (866) 217-9197 (toll free).

Reviewer: Keisha Douglas

Timestamp: [year=2009; month=3; day=23; hr=16; min=5; sec=4; ms=599;]

Validated By CRFValidator v 1.0.3

Application No: 10539956 Version No: 2.0

Input Set:

Output Set:

Started: 2009-03-02 15:51:10.272 **Finished:** 2009-03-02 15:51:13.674

Elapsed: 0 hr(s) 0 min(s) 3 sec(s) 402 ms

Total Warnings: 16
Total Errors: 0

No. of SeqIDs Defined: 107

Actual SeqID Count: 107

Erro	or code	Error Descript	ion								
W	213	Artificial	or	Unknown	found	in	<213>	in	SEQ	ID	(21)
W	213	Artificial	or	Unknown	found	in	<213>	in	SEQ	ID	(22)
W	213	Artificial	or	Unknown	found	in	<213>	in	SEQ	ID	(23)
W	213	Artificial	or	Unknown	found	in	<213>	in	SEQ	ID	(24)
W	213	Artificial	or	Unknown	found	in	<213>	in	SEQ	ID	(25)
W	213	Artificial	or	Unknown	found	in	<213>	in	SEQ	ID	(26)
W	213	Artificial	or	Unknown	found	in	<213>	in	SEQ	ID	(27)
W	213	Artificial	or	Unknown	found	in	<213>	in	SEQ	ID	(98)
W	213	Artificial	or	Unknown	found	in	<213>	in	SEQ	ID	(99)
W	213	Artificial	or	Unknown	found	in	<213>	in	SEQ	ID	(100)
W	213	Artificial	or	Unknown	found	in	<213>	in	SEQ	ID	(101)
W	213	Artificial	or	Unknown	found	in	<213>	in	SEQ	ID	(102)
W	213	Artificial	or	Unknown	found	in	<213>	in	SEQ	ID	(103)
W	213	Artificial	or	Unknown	found	in	<213>	in	SEQ	ID	(104)
W	213	Artificial	or	Unknown	found	in	<213>	in	SEQ	ID	(105)
W	213	Artificial	or	Unknown	found	in	<213>	in	SEQ	ID	(107)

<150> PCT/US03/041182 <151> 2003-12-22 <150> 60/435,077

<151> 2002-12-20

<160> 107

<170> PatentIn Ver. 2.1

<210> 1 <211> 1227 <212> DNA <213> Borrelia burgdorferi <220>

<221> CDS <222> (75)..(1142)

<400> 1

acctacactt gttaaaactc tctttttgag ttaagatgat aacttatact tttcattata 60

aggagacgat gaat atg aaa aaa att tca agt gca agt tta tta aca act 110

Met Lys Lys Ile Ser Ser Ala Ser Leu Leu Thr Thr

1 5 10

ttc ttt gtt ttt att aat tgt aaa agc caa gtt gct gat aag gac gac 158
Phe Phe Val Phe Ile Asn Cys Lys Ser Gln Val Ala Asp Lys Asp Asp
15 20 25

cca aca aac aaa ttt tac caa tct gtc ata caa tta ggt aac gga ttt 206
Pro Thr Asn Lys Phe Tyr Gln Ser Val Ile Gln Leu Gly Asn Gly Phe
30 35 40

ctt gat gta ttc aca tct ttt ggt ggg tta gta gca gag gct ttt gga 254 Leu Asp Val Phe Thr Ser Phe Gly Gly Leu Val Ala Glu Ala Phe Gly 45 55 60

ttt aaa tca gat cca aaa aaa tct gat gta aaa acc tat ttt act act 302
Phe Lys Ser Asp Pro Lys Lys Ser Asp Val Lys Thr Tyr Phe Thr Thr
65 70 75

gta gct gcc aaa ttg gaa aaa aca aaa acc gat ctt aat agt ttg cct 350 Val Ala Ala Lys Leu Glu Lys Thr Lys Thr Asp Leu Asn Ser Leu Pro

80 85 90

_	-		_	_		_	_	_	_	Gly			-	_		398
		-			-	-			-	att Ile	_	-	-	-		446
_	_	-	_	_	-		_	-	_	aca Thr 135	_			-		494
-			-	-			-	-		gct Ala	-	-	-	-	-	542
_	-	-	_	_		_		_		att Ile	-	_			_	590
										aag Lys						638
_	-								-	gly	_	_			-	686
-		-	-	-			-	-		gct Ala 215	_	-	_		_	734
	-	_	_	_	-	_			_	ata Ile		-			_	782
_	-	-	-		-		_	-		aag Lys	_				-	830
		_		_	-	_			-	aaa Lys	-					878
		_	_		_	_	_	-	-	cag Gln		-	-	_		926
-	_			_	-	_	-		_	ttt Phe 295	-		_	-		974
			_	_			_		_	gga Gly	_	-			_	1022

			gtt Val 320													1070
			cta Leu													1118
-			cct Pro	-	_		_	tgat	ittaa	att a	aagto	gtato	gg ad	cacga	actat	1172
gcco	ctcat	iga t	tgaq	ggaaa	at aç	gtega	agaga	a tat	atat	act	aaaa	agat	aat a	aaata	a	1227
<212	L> 35 2> PE	RT	lia k	ourgo	dorf∈	eri										
<400 Met 1		Lys	Ile	Ser 5	Ser	Ala	Ser	Leu	Leu 10	Thr	Thr	Phe	Phe	Val 15	Phe	
Ile	Asn	Cys	Lys 20	Ser	Gln	Val	Ala	Asp 25	Lys	Asp	Asp	Pro	Thr 30	Asn	Lys	
Phe	Tyr	Gln 35	Ser	Val	Ile	Gln	Leu 40	Gly	Asn	Gly	Phe	Leu 45	Asp	Val	Phe	
Thr	Ser 50	Phe	Gly	Gly	Leu	Val 55	Ala	Glu	Ala	Phe	Gly 60	Phe	Lys	Ser	Asp	
Pro 65	Lys	Lys	Ser	Asp	Val 70	Lys	Thr	Tyr	Phe	Thr 75	Thr	Val	Ala	Ala	Lys 80	
Leu	Glu	Lys	Thr	Lys 85	Thr	Asp	Leu	Asn	Ser 90	Leu	Pro	Lys	Glu	Lys 95	Ser	
Asp	Ile	Ser	Ser 100	Thr	Thr	Gly	Lys	Pro 105	Asp	Ser	Thr	Gly	Ser 110	Val	Gly	
Thr	Ala	Val 115	Glu	Gly	Ala	Ile	Lys 120	Glu	Val	Ser	Glu	Leu 125	Leu	Asp	Lys	
Leu	Val 130	Lys	Ala	Val	Lys	Thr 135	Ala	Glu	Gly	Ala	Ser 140	Ser	Gly	Thr	Ala	
Ala 145	Ile	Gly	Glu	Val	Val 150	Ala	Asp	Ala	Asp	Ala 155	Ala	Lys	Val	Ala	Asp 160	
Lys	Ala	Ser	Val	Lys 165	Gly	Ile	Ala	Lys	Gly 170	Ile	Lys	Glu	Ile	Val 175	Glu	
Ala	Ala	Gly	Gly 180	Ser	Glu	Lys	Leu	Lys 185	Ala	Val	Ala	Ala	Ala 190	Lys	Gly	

Glu Asn Asn Lys	Gly Ala G	ly Lys Leu 200	Phe Gly Lys	Ala Gly Ala 205	Ala
Ala His Gly Asp		la Ala Ser 15	Lys Ala Ala 220	Gly Ala Val	Ser
Ala Val Ser Gly 225	Glu Gln I 230	le Leu Ser	Ala Ile Val 235	Thr Ala Ala	Asp 240
Ala Ala Glu Glr	Asp Gly L	ys Lys Pro	Glu Glu Ala 250	Lys Asn Pro 255	Ile
Ala Ala Ala Ile		ys Asp Gly 265	Gly Ala Glu	Phe Gly Gln 270	Asp
Glu Met Lys Lys 275	. Asp Asp G	ln Ile Ala 280	Ala Ala Ile	Ala Leu Arg 285	Gly
Met Ala Lys Asp 290		he Ala Val 95	Lys Asp Gly 300	Glu Lys Glu	Lys
Ala Glu Gly Ala	a Ile Lys G 310	ly Ala Ala	Glu Ser Ala 315	Val Arg Lys	Val 320
Leu Gly Ala Ile	Thr Gly L	eu Ile Gly	Asp Ala Val	Ser Ser Gly 335	Leu
Arg Lys Val Gly	_	al Lys Ala 345	Ala Ser Lys	Glu Thr Pro 350	Pro
Ala Leu Asn Lys	3				
<210> 3 <211> 1141 <212> DNA <213> Borrelia	hermsii				
<220> <221> CDS <222> (1)(106	52)				
<400> 3 atg aga aaa aga	ı ata agt g	ca ata ata	atg act tta	ttt atg gta	tta 48
Met Arg Lys Arc	g Ile Ser A 5	la Ile Ile	Met Thr Leu 10	Phe Met Val	Leu
gta agc tgt aat Val Ser Cys Asr 20	Ser Gly G				
tta aca tct ata Leu Thr Ser Ile 35	_				
act ttt gga gat	atg gtt a	ct gga gct	ttt ggt att	aag gca gat	act 192

Thr	Phe 50	Gly	Asp	Met	Val	Thr 55	Gly	Ala	Phe	Gly	Ile 60	Lys	Ala	Asp	Thr	
_		_	-	_		_				-	_	gag Glu	-		_	240
		-		_	_	-		-	-	-	-	aag Lys				288
		_		_		-		_	-		_	gca Ala	_			336
_					-		-	-				gct Ala 125			-	384
_						_	_			_	_	gta Val			_	432
_		_	-				-					gaa Glu		-		480
_	-	_	_	_		_	_	_	-	_	_	act Thr		_	_	528
_	_		_							-		act Thr	-			576
_	-	_			-	-		_	-	-		tca Ser 205			_	624
			_	_		-		_		_		tct Ser	_	_		672
	-	_		_		-			-		_	aca Thr	-	_	_	720
		_	_	_		_		_				gag Glu			_	768
	-			-	-	-		-	-			gca Ala	_	_	-	816
atg	gct	aag	aat	ggt	aca	ttt	tct	att	aaa	aac	aat	gaa	gat	gcg	gct	864

Met Ala Lys Asn Gly Thr Phe Ser Ile Lys Asn Asn Glu Asp Ala Ala

275 280 285

_	_	_			-	-	_	gca Ala	-	-			_			912
-					-			aat Asn		_	_	_				960
				-		-		gtt Val			_	_			_	1008
_	_				_	-	_	aca Thr 345		_		_				1056
aac Asn	tag	ttaa	agggt	aa a	atata	aaag	ga ta	aaagt	tati	t gta	aagg	gaaa	agct	ttt	ctt	1112
gttt	ttaa	atg (cagga	aatgt	a gt	ttct	ctg									1141
<212	0> 4 L> 35 2> PE 3> Bo	RT	lia 1	nerms	sii											
< 400)> 4															
		Lys	Arg	Ile	Ser	Ala	Ile	Ile	Met	Thr	Leu	Phe	Met	Val	Leu	
1				5					10					15		
Val	Ser	Cys	Asn 20	Ser	Gly	Gly	Val	Ala 25	Glu	Asp	Pro	Lys	Thr 30	Val	Tyr	
Leu	Thr	Ser 35	Ile	Ala	Asn	Leu	Gly 40	Làs	Gly	Phe	Leu	Asp 45	Val	Phe	Val	
Thr	Phe 50	Gly	Asp	Met	Val	Thr 55	Gly	Ala	Phe	Gly	Ile 60	Lys	Ala	Asp	Thr	
Lys 65	Lys	Ser	Asp	Ile	Gly 70	Lys	Tyr	Phe	Thr	Asp 75	Ile	Glu	Ser	Thr	Met 80	
Thr	Ser	Val	Lys	Lys 85	Lys	Leu	Gln	Asp	Glu 90	Val	Ala	Lys	Asn	Gly 95	Asn	
Tyr	Pro	Lys	Val 100	Lys	Thr	Ala	Val	Asp 105	Glu	Phe	Val	Ala	Ile 110	Leu	Gly	
Lys	Ile	Glu 115	Lys	Gly	Ala	Lys	Glu 120	Ala	Ser	Lys	Gly	Ala 125	Thr	Gly	Asp	
Val	Ile 130	Ile	Gly	Asn	Thr	Val 135	Lys	Asn	Gly	Asp	Ala 140	Val	Pro	Gly	Glu	
Ala 145	Thr	Ser	Val	Asn	Ser 150	Leu	Val	Lys	Gly	Ile 155	Lys	Glu	Ile	Val	Gly 160	
Val	Val	Leu	Lys	Glu 165	Gly	Lys	Ala	Asp	Ala 170	Asp	Ala	Thr	Lys	Asp 175	Asp	
Ser	Lys	Lys	Asp 180		Gly	Lys	Leu	Phe		Ala	Thr	Thr	Asp		Asn	
Arg	Ala	Asp		Ala	Ala	Ala	Gln 200	Ala	Ala	Ala	Ala	Ser 205		Gly	Ala	

Val Thr Gly Ala Asp Ile Leu Gln Ala Ile Val Gln Ser Lys Glu Asn

	210					215					220					
Pro	Val	Ala	Asn	Ser	Thr	Asp	Gly	Ile	Glu	Lys	Ala	Thr	Asp	Ala	Ala	
225					230					235					240	
Glu	Ile	Ala	Val	Ala	Pro	Ala	Lys	Asp	Asn	Lys	Lys	Glu	Ile	Lys	Asp	
				245					250					255		
Glv	Ala	Lvs	Lvs	Asp	Ala	Val	Ile	Ala	Ala	Glv	Ile	Ala	Leu	Ara	Ala	
			260					265					270			
Mot	Ala	Tva		Gl _v	Thr	Dho	Sor		Tva	Λan	Λan	Glu		Δla	Λla	
riec	лта	275	ASII	Gry	TILL	FILE	280	116	шуз	ASII	ASII	285	дър	лта	AIA	
7	m1		- 1		a	- 1		- 1	a	- 1	7		-	- 1	_	
vai	Thr	ınr	TIE	Asn	ser		Ата	АІА	ser	Ата		Asn	гуѕ	TTE	Leu	
	290					295					300					
Ser	Thr	Leu	Ile	Ile		Ile	Arg	Asn	Thr		Asp	Ser	Gly	Leu	Lys	
305					310					315					320	
Thr	Ile	Asn	Glu	Ala	Leu	Ala	Thr	Val	Lys	Gln	Glu	Asp	TA2	Ser	Val	
				325					330					335		
Glu	Ala	Thr	Asn	Thr	Ala	Glu	Ala	Thr	Thr	Ser	Gly	Gln	Gln	Ala	Lys	
			340					345					350			
Asn																
<210	0> 5															
	1> 41	16														
	2> D1															
<21.	3> Bo	orrel	lia a	aize.	Lll											
<220	O>															
	0> 1> CI	os														
<221			(414)	ı												
<221	l> CI		(414)													
<221 <221	l> CI		(414)	ı												
<222 <222 <400	1> CI 2> (1	L)			aaa	ata	aag	ggg	att	gtt	gcg	gct	gct	ggg	aag	48
<222 <222 <400 aag	1> CI 2> (1 0> 5	l)	gcg	aag			_			-		-	-		_	48
<222 <222 <400 aag Lys	1> CI 2> (1 0> 5 ggg	l)	gcg	aag			_		Ile	-		-	-	Gly	_	48
<222 <222 <400 aag	1> CI 2> (1 0> 5 ggg	l)	gcg	aag Lys			_			-		-	-		_	48
<222 <222 <400 aag Lys	1> CI 2> (1 0> 5 ggg Gly	att	gcg Ala	aag Lys 5	Gly	Ile	Lys	Gly	Ile 10	Val	Ala	Ala	Ala	Gly 15	Lys	
<222 <222 <400 aag Lys 1	1> CI 2> (1 0> 5 ggg Gly	att Ile	gcg Ala	aag Lys 5 gat	Gly	Ile gat	dcd	Gly	Ile 10 aca	Val ggt	Ala	Ala	Ala	Gly 15 gct	Lys	48
<222 <222 <400 aag Lys 1	1> CI 2> (1 0> 5 ggg Gly	att Ile	gcg Ala aag Lys	aag Lys 5 gat	Gly	Ile gat	dcd	Gly ctg Leu	Ile 10 aca	Val ggt	Ala	Ala	Ala aaa Lys	Gly 15 gct	Lys	
<222 <222 <400 aag Lys 1	1> CI 2> (1 0> 5 ggg Gly	att Ile	gcg Ala	aag Lys 5 gat	Gly	Ile gat	dcd	Gly	Ile 10 aca	Val ggt	Ala	Ala	Ala	Gly 15 gct	Lys	
<222 <222 <400 aag Lys 1 gct Ala	1> CI 2> (3 0> 5 ggg Gly ttt Phe	att Ile ggc Gly	gcg Ala aag Lys 20	aag Lys 5 gat Asp	Gly ggt Gly	Ile gat Asp	Lys gcg Ala	Gly ctg Leu 25	Ile 10 aca Thr	Val ggt Gly	Ala gtt Val	Ala gca Ala	Ala aaa Lys 30	Gly 15 gct Ala	Lys gct Ala	96
<222 <222 <400 aag Lys 1 gct Ala	1> CI 2> (1 0> 5 ggg Gly	att Ile ggc Gly	gcg Ala aag Lys 20	aag Lys 5 gat Asp	Gly ggt Gly	Ile gat Asp	Lys gcg Ala	Gly ctg Leu 25	Ile 10 aca Thr	Val ggt Gly	Ala gtt Val	Ala gca Ala	Ala aaa Lys 30	Gly 15 gct Ala	Lys gct Ala	
<222 <222 <400 aag Lys 1 gct Ala	1> CI 2> (3 0> 5 ggg Gly ttt Phe	att Ile ggc Gly	gcg Ala aag Lys 20	aag Lys 5 gat Asp	Gly ggt Gly	Ile gat Asp	Lys gcg Ala	Gly ctg Leu 25	Ile 10 aca Thr	Val ggt Gly	Ala gtt Val	Ala gca Ala gct	Ala aaa Lys 30	Gly 15 gct Ala	Lys gct Ala	96
<222 <222 <400 aag Lys 1 gct Ala	1> CI 2> (1) 0> 5 ggg Gly ttt Phe	att Ile ggc Gly	gcg Ala aag Lys 20	aag Lys 5 gat Asp	Gly ggt Gly	Ile gat Asp	Lys gcg Ala	Gly ctg Leu 25	Ile 10 aca Thr	Val ggt Gly	Ala gtt Val	Ala gca Ala gct	Ala aaa Lys 30	Gly 15 gct Ala	Lys gct Ala	96
<222 <222 <400 aag Lys 1 gct Ala	1> CI 2> (1) 0> 5 ggg Gly ttt Phe	att Ile ggc Gly gat Asp	gcg Ala aag Lys 20	aag Lys 5 gat Asp	Gly ggt Gly	Ile gat Asp	Lys gcg Ala gcg Ala	Gly ctg Leu 25	Ile 10 aca Thr	Val ggt Gly	Ala gtt Val	Ala gca Ala gct Ala	Ala aaa Lys 30	Gly 15 gct Ala	Lys gct Ala	96
<221 <222 <400 aag Lys 1 gct Ala gag Glu	1> CI 2> (1) 0> 5 ggg Gly ttt Phe	att Ile ggc Gly gat Asp 35	gcg Ala aag Lys 20 gct Ala	aag Lys 5 gat Asp aac Asn	Gly ggt Gly aag Lys	Ile gat Asp gat Asp	Lys gcg Ala gcg Ala 40	Gly ctg Leu 25 ggg Gly	Ile 10 aca Thr aag Lys	Val ggt Gly ttg Leu	Ala gtt Val ttt Phe	Ala gca Ala gct Ala 45	Ala aaa Lys 30 ggt Gly	Gly 15 gct Ala aag Lys	Lys gct Ala aat Asn	96
<222 <400 aag Lys 1 gct Ala gag Glu	1> CI 2> (1 0> 5 ggg Gly ttt Phe	att Ile ggc Gly gat Asp 35	gcg Ala aag Lys 20 gct Ala	aag Lys 5 gat Asp aac Asn	Gly ggt Gly aag Lys	gat Asp gat Asp	Lys gcg Ala gcg Ala 40	Gly ctg Leu 25 ggg Gly	Ile 10 aca Thr aag Lys	Val ggt Gly ttg Leu gcg	Ala gtt Val ttt Phe	Ala gca Ala gct Ala 45	Ala aaa Lys 30 ggt Gly	Gly 15 gct Ala aag Lys	Lys gct Ala aat Asn	96
<222 <400 aag Lys 1 gct Ala gag Glu	1> CI 2> (1 0> 5 ggg Gly ttt Phe aat Asn	att Ile ggc Gly gat Asp 35	gcg Ala aag Lys 20 gct Ala	aag Lys 5 gat Asp aac Asn	Gly ggt Gly aag Lys	gat Asp gat Asp	Lys gcg Ala gcg Ala 40	Gly ctg Leu 25 ggg Gly	Ile 10 aca Thr aag Lys	Val ggt Gly ttg Leu gcg	Ala gtt Val ttt Phe	Ala gca Ala gct Ala 45	Ala aaa Lys 30 ggt Gly	Gly 15 gct Ala aag Lys	Lys gct Ala aat Asn	96
<222 <400 aag Lys 1 gct Ala gag Glu	1> CI 2> (: 0> 5 ggg Gly ttt Phe aat Asn	att Ile ggc Gly gat Asp 35	gcg Ala aag Lys 20 gct Ala	aag Lys 5 gat Asp aac Asn	Gly ggt Gly aag Lys	gat Asp gat Asp gac Asp	Lys gcg Ala gcg Ala 40	Gly ctg Leu 25 ggg Gly	Ile 10 aca Thr aag Lys	Val ggt Gly ttg Leu gcg	Ala gtt Val ttt Phe	Ala gca Ala gct Ala 45	Ala aaa Lys 30 ggt Gly	Gly 15 gct Ala aag Lys	Lys gct Ala aat Asn	96
<222 <400 aag Lys 1 gct Ala gag Glu	1> CI 2> (1 0> 5 ggg Gly ttt Phe aat Asn 50	att Ile ggc Gly gat Asp 35 gct Ala	gcg Ala aag Lys 20 gct Ala ggt Gly	aag Lys 5 gat Asp aac Asn	Gly ggt Gly aag Lys gct Ala	gat Asp gat Asp gac Asp 55	Lys gcg Ala gcg Ala 40 att Ile	Gly ctg Leu 25 ggg Gly gcg Ala	Ile 10 aca Thr aag Lys	yal ggt Gly ttg Leu gcg Ala	Ala gtt Val ttt Phe gct Ala 60	Ala gca Ala gct Ala 45 gct Ala	Ala aaa Lys 30 ggt Gly gct Ala	Gly 15 gct Ala aag Lys gtt Val	Lys gct Ala aat Asn act Thr	96 144 192
<222 <400 aag Lys 1 gct Ala gag Glu ggt	1> CI 2> (1 0> 5 ggg Gly ttt Phe aat Asn 50 gtt	att Ile ggc Gly gat Asp 35 gct Ala	gcg Ala aag Lys 20 gct Ala ggt Gly	aag Lys 5 gat Asp aac Asn	Gly ggt Gly aag Lys gct Ala	gat Asp gat Asp gac Asp 55	Lys gcg Ala gcg Ala 40 att Ile	Gly ctg Leu 25 ggg Gly gcg Ala	Ile 10 aca Thr aag Lys aag Lys	Val ggt Gly ttg Leu gcg Ala	Ala gtt Val ttt Phe gct Ala 60	Ala gca Ala gct Ala 45 gct Ala	Ala aaa Lys 30 ggt Gly gct Ala	Gly 15 gct Ala aag Lys gtt Val	gct Ala aat Asn act Thr	96
<222 <400 aag Lys 1 gct Ala gag Glu ggt Gly	1> CI 2> (1 0> 5 ggg Gly ttt Phe aat Asn 50	att Ile ggc Gly gat Asp 35 gct Ala	gcg Ala aag Lys 20 gct Ala ggt Gly	aag Lys 5 gat Asp aac Asn	Gly ggt Gly aag Lys gct Ala cag Gln	gat Asp gat Asp gac Asp 55	Lys gcg Ala gcg Ala 40 att Ile	Gly ctg Leu 25 ggg Gly gcg Ala	Ile 10 aca Thr aag Lys aag Lys	Val ggt Gly ttg Leu gcg Ala att	Ala gtt Val ttt Phe gct Ala 60	Ala gca Ala gct Ala 45 gct Ala	Ala aaa Lys 30 ggt Gly gct Ala	Gly 15 gct Ala aag Lys gtt Val	Lys gct Ala aat Asn act Thr	96 144 192
<222 <400 aag Lys 1 gct Ala gag Glu ggt	1> CI 2> (1 0> 5 ggg Gly ttt Phe aat Asn 50 gtt	att Ile ggc Gly gat Asp 35 gct Ala	gcg Ala aag Lys 20 gct Ala ggt Gly	aag Lys 5 gat Asp aac Asn	Gly ggt Gly aag Lys gct Ala	gat Asp gat Asp gac Asp 55	Lys gcg Ala gcg Ala 40 att Ile	Gly ctg Leu 25 ggg Gly gcg Ala	Ile 10 aca Thr aag Lys aag Lys	Val ggt Gly ttg Leu gcg Ala	Ala gtt Val ttt Phe gct Ala 60	Ala gca Ala gct Ala 45 gct Ala	Ala aaa Lys 30 ggt Gly gct Ala	Gly 15 gct Ala aag Lys gtt Val	gct Ala aat Asn act Thr	96 144 192
<222 <400 aag Lys 1 gct Ala gag Glu ggt Gly	1> CI 2> (1 0> 5 ggg Gly ttt Phe aat Asn 50 gtt	att Ile ggc Gly gat Asp 35 gct Ala	gcg Ala aag Lys 20 gct Ala ggt Gly	aag Lys 5 gat Asp aac Asn	Gly ggt Gly aag Lys gct Ala cag Gln	gat Asp gat Asp gac Asp 55	Lys gcg Ala gcg Ala 40 att Ile	Gly ctg Leu 25 ggg Gly gcg Ala	Ile 10 aca Thr aag Lys aag Lys	Val ggt Gly ttg Leu gcg Ala att	Ala gtt Val ttt Phe gct Ala 60	Ala gca Ala gct Ala 45 gct Ala	Ala aaa Lys 30 ggt Gly gct Ala	Gly 15 gct Ala aag Lys gtt Val	Lys gct Ala aat Asn act Thr	96 144 192
<222 <222 <400 aag Lys 1 gct Ala gag Glu ggt Gly gcg Ala 65	1> CI 2> (1 0> 5 ggg Gly ttt Phe aat Asn 50 gtt	att Ile ggc Gly gat Asp 35 gct Ala	gcg Ala aag Lys 20 gct Ala ggt Gly	aag Lys 5 gat Asp aac Asn gct Ala	Gly ggt Gly aag Lys gct Ala cag Gln 70	gat Asp gat Asp 55 ata Ile	gcg Ala gcg Ala 40 att Ile cta Leu	Gly ctg Leu 25 ggg Gly gcg Ala aaa Lys	Ile 10 aca Thr aag Lys aag Lys gct Ala	ggt Gly ttg Leu gcg Ala att Ile 75	gtt Val ttt Phe gct Ala 60 gtt Val	Ala gca Ala gct Ala 45 gct Ala gct Ala	Ala aaa Lys 30 ggt Gly gct Ala gcg Ala	Gly 15 gct Ala aag Lys gtt Val	gct Ala aat Asn act Thr ggt Gly 80	96 144 192

Asp Ala Asp Gln Ala Gly Val Lys Ala Asp Ala